Sequence Search Summary

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 10, 2003; 10:05:27 ; Search time 1382 Seconds
                                         (without alignments)
                                         9413.136 Million cell updates/sec

Title: US-09-942-407-1
Perfect score: 447
Sequence: 1 atgagtaatgaggatctttt..........cccagtacccgaagaactga 447

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%   SEQ ID NO:1
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*
                 15: em_ba:*
                 16: em_fun:*
                 17: em_hum:*
                 18: em_in:*
                 19: em_mu:*
                 20: em_om:*
                 21: em_or:*
                 22: em_ov:*
                 23: em_pat:*
                 24: em_ph:*
                 25: em_pl:*
                 26: em_ro:*
                 27: em_sts:*

```
                  28:  em_un:*
                  29:  em_vi:*
                  30:  em_htg_hum:*
                  31:  em_htg_inv:*
                  32:  em_htg_other:*
                  33:  em_htg_mus:*
                  34:  em_htg_pln:*
                  35:  em_htg_rod:*
                  36:  em_htg_mam:*
                  37:  em_htg_vrt:*
                  38:  em_sy:*
                  39:  em_htgo_hum:*
                  40:  em_htgo_mus:*
                  41:  em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	447	100.0	447	1	AY046899	AY046899 Propionib
	2	447	100.0	447	6	AX128594	AX128594 Sequence
	3	447	100.0	833	1	AF454511	AF454511 Propionib
c	4	131.8	29.5	30253	1	SC8F4	AL137242 Streptomy
	5	122.2	27.3	453	6	AX121431	AX121431 Sequence
c	6	122.2	27.3	333150	1	AP005277	AP005277 Corynebac
c	7	122.2	27.3	349980	6	AX127147	AX127147 Sequence
c	8	93	20.8	17963	1	AE007009	AE007009 Mycobacte
c	9	93	20.8	32514	1	MTCY130	Z73902 Mycobacteri
	10	93	20.8	37036	1	MSGY151	AD000018 Mycobacte
	11	87.2	19.5	36470	1	U00014	U00014 Mycobacteri
c	12	87.2	19.5	332450	1	MLEPRTN5	AL583921 Mycobacte
	13	72.8	16.3	12249	1	AE002039	AE002039 Deinococc
c	14	62.4	14.0	10670	1	AE005001	AE005001 Halobacte
c	15	57.2	12.8	10262	1	AE005867	AE005867 Caulobact
	16	56.6	12.7	1288	6	AR007563	AR007563 Sequence
c	17	56.6	12.7	11477	1	AE009554	AE009554 Brucella
	18	53.8	12.0	1401	3	ACU29610	U29610 Acanthaoeba
c	19	53.8	12.0	45335	1	SCC57A	AL136519 Streptomy
c	20	52	11.6	190050	1	AL646080	AL646080 Ralstonia
c	21	50.8	11.4	65140	6	AX211705	AX211705 Sequence
c	22	50.8	11.4	113193	1	AF357202	AF357202 Streptomy
c	23	50.8	11.4	123580	1	AF263912	AF263912 Streptomy
c	24	50.8	11.4	125401	6	AX211739	AX211739 Sequence
	25	50.4	11.3	167350	2	AC129717	AC129717 Oryza sat
	26	50.4	11.3	299350	1	SME591786	AL591786 Sinorhizo
	27	50.2	11.2	13367	1	AE005105	AE005105 Halobacte
	28	49.6	11.1	1220	8	MZETASSELS	L20621 Zea mays al
	29	49.6	11.1	1236	6	AR007558	AR007558 Sequence
c	30	49.6	11.1	205050	1	AL646082	AL646082 Ralstonia
	31	49.2	11.0	982	8	AF377767	AF377767 Zea mays
	32	49.2	11.0	1018	8	AF377747	AF377747 Zea mays
	33	49.2	11.0	1018	8	AF377757	AF377757 Zea mays

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OM nucleic - nucleic search, using sw model

Run on: June 10, 2003, 09:04:31 ; Search time 179 Seconds
                                          (without alignments)
                                          5623.705 Million cell updates/sec

Title: US-09-942-407-1
Perfect score: 447
Sequence: 1 atgagtaatgaggatctttt..........cccagtacccgaagaactga 447

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_101002:*
                 1:   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
                 2:   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
                 3:   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
                 4:   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
                 5:   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
                 6:   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
                 7:   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
                 8:   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
                 9:   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
                 10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
                 11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
                 12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
                 13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
                 14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
                 15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
                 16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
                 17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
                 18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
                 19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
                 20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
                 21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
                 22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
                 23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
                 24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	447	100.0	447	22	AAH19868	Propionibacterium
	2	122.2	27.3	453	22	AAH66312	C glutamicum codin
c	3	122.2	27.3	349980	22	AAH68528	C glutamicum codin
	4	110.8	24.8	9407	23	AAS59606	Propionibacterium
c	5	93	20.8	4403765	22	AAI99683	Mycobacterium tube
c	6	93	20.8	4411529	22	AAI99682	Mycobacterium tube
	7	51.4	11.5	644	21	AAC44798	Zea mays DNA fragm
c	8	50.8	11.4	65140	22	AAD17184	Streptomyces nours
c	9	50.8	11.4	125401	22	AAD17186	Streptomyces nours
	10	49.6	11.1	1236	16	AAT45060	Maize Ts2 cDNA nuc
c	11	47.8	10.7	21185	21	AAA63350	Streptomyces globi
c	12	47.8	10.7	63164	21	AAA63348	Streptomyces globi
	13	47.4	10.6	1620	13	AAQ22482	groEL-1 gene codin
	14	47.4	10.6	2167	13	AAQ22484	gro es el operon w
	15	47.4	10.6	2668	13	AAQ22485	groEL-1 gene. Str
c	16	47.2	10.6	88421	24	AAL40781	88421nt genomic DN
	17	46.4	10.4	6781	19	AAV45824	Maize phosphenolpy
	18	45.8	10.2	1320	13	AAQ22481	groEL-1 gene parti
c	19	45	10.1	77536	21	AAA14651	Nucleotide sequenc
	20	44.6	10.0	970	24	AAI69374	Streptomyces sp L-
	21	44.6	10.0	2061	24	AAI69367	Streptomyces sp L-
	22	44.2	9.9	852	24	ABA99451	Actinoplanes sp DN
	23	44.2	9.9	38064	24	ABA99469	Actinoplanes sp SE
	24	44	9.8	4044	12	AAQ15154	Plasmid pHAS2-MCP
	25	43.8	9.8	7559	20	AAV82011	Maize phosphoenolp
	26	43	9.6	1011	24	ABL88001	DNA polymerase III
	27	43	9.6	1011	24	ABL88002	DNA polymerase III
	28	43	9.6	1140	24	ABL61289	N. uniformis p-hyd
	29	42.4	9.5	58857	21	AAA58471	Nucleotide sequenc
	30	42.4	9.5	4411529	22	AAI99682	Mycobacterium tube
	31	42.2	9.4	699	23	AAS51514	Pseudomonas aerugi
	32	42.2	9.4	3978	21	AAC55785	Type I polyketide
	33	42.2	9.4	12249	21	AAC55840	Complete Mitomycin
	34	42.2	9.4	18331	21	AAC55857	Complete nucleotid
	35	42	9.4	44377	18	AAT78508	Platenolide syntha
	36	42	9.4	44377	18	AAT80414	Platenolide syntha
c	37	41.8	9.4	894	23	AAS51512	Pseudomonas aerugi
	38	41.6	9.3	3059	8	AAN70566	Sequence encoding
	39	41.6	9.3	7110	22	AAF81361	Quorum sensing con
	40	41.4	9.3	4403765	22	AAI99683	Mycobacterium tube
	41	41.2	9.2	5836	23	AAS86905	DNA encoding novel
	42	41	9.2	2302	21	AAA15621	Human heat shock p
	43	40.8	9.1	2602	24	ABK27559	DNA encoding Chlam
	44	40.8	9.1	3993	12	AAQ15153	Swine herpes virus
	45	40.8	9.1	65140	22	AAD17184	Streptomyces nours

ALIGNMENTS

RESULT 1

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OM nucleic - nucleic search, using sw model

Run on: June 10, 2003, 10:56:32 ; Search time 118 Seconds
                                          (without alignments)
                                          5301.637 Million cell updates/sec

Title: US-09-942-407-1
Perfect score: 447
Sequence: 1 atgagtaatgaggatctttt..........cccagtacccgaagaactga 447

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
                  1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                  2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                  3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                  4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                  5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                  6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                  7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                  8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                  9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                  10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
                  11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                  12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
                  13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                  14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query
  No.   Score   Match Length DB   ID   Description
  ----
       1   447 100.0   447   10 US-09-942-407-1   Sequence 1, Appli
       2 122.2   27.3   453   9 US-09-738-626-1347   Sequence 1347, Ap
  c   3 122.2   27.3 3309400   9 US-09-738-626-1   Sequence 1, Appli

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OM nucleic - nucleic search, using sw model

Run on: June 10, 2003, 10:06:57 ; Search time 1140 Seconds
                                           (without alignments)
                                           6350.336 Million cell updates/sec

Title: US-09-942-407-1
Perfect score: 447
Sequence: 1 atgagtaatgaggatctttt..........cccagtacccgaagaactga 447

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1: em_estba:*
                 2: em_esthum:*
                 3: em_estin:*
                 4: em_estmu:*
                 5: em_estov:*
                 6: em_estpl:*
                 7: em_estro:*
                 8: em_htc:*
                 9: gb_est1:*
                 10: gb_est2:*
                 11: gb_htc:*
                 12: gb_est3:*
                 13: gb_est4:*
                 14: gb_est5:*
                 15: em_estfun:*
                 16: em_estom:*
                 17: gb_gss:*
                 18: em_gss_hum:*
                 19: em_gss_inv:*
                 20: em_gss_pln:*
                 21: em_gss_vrt:*
                 22: em_gss_fun:*
                 23: em_gss_mam:*
                 24: em_gss_mus:*
                 25: em_gss_other:*
                 26: em_gss_pro:*
                 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	56.2	12.6	582	13	BM356337	BM356337 kx63a05.y
	2	51.8	11.6	670	12	BG847251	BG847251 1024016E0
	3	50.6	11.3	539	13	BM135667 ·	BM135667 WHE2622_F
	4	50.6	11.3	574	14	BQ838343	BQ838343 WHE2909_D
	5	50	11.2	527	10	BE430090	BE430090 TAS006.H1
	6	50	11.2	547	14	BQ240794	BQ240794 TaE05012G
c	7	47.4	10.6	1133	17	CNS06RLZ	AL412125 T7 end of
	8	47	10.5	381	10	AV629941	AV629941 AV629941
	9	47	10.5	490	10	AV642714	AV642714 AV642714
	10	47	10.5	525	13	BM000766	BM000766 1031091A1
	11	47	10.5	536	13	BI727253	BI727253 1031091A1
c	12	46.4	10.4	925	17	CNS0091P	AL053013 Drosophil
	13	46	10.3	850	10	BE194762	BE194762 HVSMEh008
	14	45.8	10.2	426	13	BI779862	BI779862 EBem07_SQ
	15	45.8	10.2	768	13	BI999409	BI999409 1031073E0
	16	45.8	10.2	866	12	BG368927	BG368927 HVSMEi002
	17	45.8	10.2	944	12	BG122847	BG122847 602348922
	18	45.6	10.2	484	10	AV619352	AV619352 AV619352
	19	45.4	10.2	504	10	BE498454	BE498454 WHE0967_F
	20	45	10.1	1304	14	BQ440317	BQ440317 AGENCOURT
	21	44.8	10.0	925	17	CNS0091P	AL053013 Drosophil
	22	44.8	10.0	1101	17	CNS017SY	AL108460 Drosophil
	23	44.8	10.0	2985	11	AY110048	AY110048 Zea mays
c	24	44.4	9.9	485	14	BQ662567	BQ662567 HS03A03u
	25	44.4	9.9	506	12	BG369860	BG369860 HVSMEi002
	26	44.4	9.9	555	12	BG909521	BG909521 TaLr1104H
	27	44.4	9.9	559	12	BG368967	BG368967 HVSMEi002
	28	44.4	9.9	587	14	BQ466460	BQ466460 HT02J12r
	29	44.4	9.9	619	12	BG368681	BG368681 HVSMEi002
	30	44.4	9.9	758	12	BG365691	BG365691 HVSMEi000
	31	44.4	9.9	855	10	BE194372	BE194372 HVSMEh008
	32	44.4	9.9	881	10	BE454755	BE454755 HVSMEh009
	33	44.2	9.9	459	13	BJ224347	BJ224347 BJ224347
	34	44.2	9.9	485	12	BF250394	BF250394 pa98f04.y
	35	44.2	9.9	494	12	BF250354	BF250354 pa98b06.y
	36	44.2	9.9	628	13	BJ281512	BJ281512 BJ281512
	37	44.2	9.9	643	9	AL828220	AL828220 AL828220
	38	44.2	9.9	645	13	BJ313569	BJ313569 BJ313569
	39	44.2	9.9	650	13	BJ268932	BJ268932 BJ268932
	40	44.2	9.9	675	13	BI723038	BI723038 1031065F0
	41 ·	44.2	9.9	679	13	BJ246201	BJ246201 BJ246201
	42	44	9.8	291	14	BQ819833	BQ819833 1030080F0
	43	44	9.8	323	10	AV639250	AV639250 AV639250
	44	44	9.8	346	10	AV388606	AV388606 AV388606
	45	44	9.8	361	10	AV397833	AV397833 AV397833

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OM nucleic - nucleic search, using sw model

Run on: June 10, 2003, 10:26:02 ; Search time 42 Seconds
                                            (without alignments)
                                            3263.917 Million cell updates/sec

Title: US-09-942-407-1
Perfect score: 447
Sequence: 1 atgagtaatgaggatctttt..........cccagtacccgaagaactga 447

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                   1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                   2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                   3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                   4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                   5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                   6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
    No.   Score   Match Length DB   ID   Description
----
c   1   93   20.8   4403765 4   US-09-103-840A-2   Sequence 2, Appli
c   2   93   20.8   4411529 4   US-09-103-840A-1   Sequence 1, Appli
    3   56.6   12.7   1288   1   US-08-440-856A-9   Sequence 9, Appli
    4   49.6   11.1   1236   1   US-08-440-856A-1   Sequence 1, Appli
    5   47.4   10.6   1320   2   US-08-461-775-8   Sequence 8, Appli
    6   47.4   10.6   1320   3   US-09-031-606-8   Sequence 8, Appli
    7   47.4   10.6   1620   2   US-08-461-775-10   Sequence 10, Appl
    8   47.4   10.6   1620   3   US-09-031-606-10   Sequence 10, Appl
    9   47.4   10.6   2167   2   US-08-461-775-9   Sequence 9, Appli
   10   47.4   10.6   2167   3   US-09-031-606-9   Sequence 9, Appli
   11   47.4   10.6   2668   2   US-08-461-775-11   Sequence 11, Appl

```
                          GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on:           June 10, 2003, 11:16:42 ; Search time 2177 Seconds
                                            (without alignments)
                                            1978.510 Million cell updates/sec

Title:            US-09-942-407-2
Perfect score:    796
Sequence:         1 MSNEDLFICIDHVAYACPDA..........FMHPKSGKGVLIELTQYPKN 148

Scoring table:    BLOSUM62
                  Xgapop 10.0 , Xgapext  0.5
                  Ygapop 10.0 , Ygapext  0.5
                  Fgapop  6.0 , Fgapext  7.0
                  Delop   6.0 , Delext   7.0
```

SEQ ID NO:2 in DNA databases (handwritten)

```
Searched:         2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters:        4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US09942407/runat_04062003_144515_9416/app_query.fasta_1.32
7
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09942407_@CGN_1_1_2496_@runat_04062003_144515_9416 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :        GenEmbl:*
                  1:  gb_ba:*
                  2:  gb_htg:*
                  3:  gb_in:*
                  4:  gb_om:*
                  5:  gb_ov:*
                  6:  gb_pat:*
                  7:  gb_ph:*
                  8:  gb_pl:*
                  9:  gb_pr:*
                  10:  gb_ro:*
```

```
       11:  gb_sts:*
       12:  gb_sy:*
       13:  gb_un:*
       14:  gb_vi:*
       15:  em_ba:*
       16:  em_fun:*
       17:  em_hum:*
       18:  em_in:*
       19:  em_mu:*
       20:  em_om:*
       21:  em_or:*
       22:  em_ov:*
       23:  em_pat:*
       24:  em_ph:*
       25:  em_pl:*
       26:  em_ro:*
       27:  em_sts:*
       28:  em_un:*
       29:  em_vi:*
       30:  em_htg_hum:*
       31:  em_htg_inv:*
       32:  em_htg_other:*
       33:  em_htg_mus:*
       34:  em_htg_pln:*
       35:  em_htg_rod:*
       36:  em_htg_mam:*
       37:  em_htg_vrt:*
       38:  em_sy:*
       39:  em_htgo_hum:*
       40:  em_htgo_mus:*
       41:  em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	796	100.0	447	1	AY046899	AY046899 Propionib
	2	796	100.0	447	6	AX128594	AX128594 Sequence
	3	796	100.0	833	1	AF454511	AF454511 Propionib
	4	358	45.0	453	6	AX121431	AX121431 Sequence
c	5	358	45.0	333150	1	AP005277	AP005277 Corynebac
c	6	358	45.0	349980	6	AX127147	AX127147 Sequence
c	7	300	37.7	30253	1	SC8F4	AL137242 Streptomy
	8	289.5	36.4	36470	1	U00014	U00014 Mycobacteri
c	9	289.5	36.4	332450	1	MLEPRTN5	AL583921 Mycobacte
c	10	266	33.4	17963	1	AE007009	AE007009 Mycobacte
c	11	266	33.4	32514	1	MTCY130	Z73902 Mycobacteri
	12	266	33.4	37036	1	MSGY151	AD000018 Mycobacte
	13	235	29.5	11261	1	AE006842	AE006842 Sulfolobu
	14	226.5	28.5	291050	1	AP000982	AP000982 Sulfolobu
c	15	219	27.5	13610	1	AE013181	AE013181 Thermoana
	16	214	26.9	13667	1	AE013084	AE013084 Thermoana

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2003, 11:15:42 ; Search time 205 Seconds
                                          (without alignments)
                                          1625.833 Million cell updates/sec

Title: US-09-942-407-2
Perfect score: 796
Sequence: 1 MSNEDLFICIDHVAYACPDA.........FMHPKSGKGVLIELTQYPKN 148

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US09942407/runat_04062003_144514_9410/app_query.fasta_1.32
7
-DB=N_Geneseq_101002 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09942407_@CGN_1_1_263_@runat_04062003_144514_9410 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   N_Geneseq_101002:*
                 1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
                 2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
                 3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
                 4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
                 5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
                 6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
                 7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
                 8: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
                 9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
                 10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*

```
11:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24:  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	796	100.0	447	22	AAH19868	Propionibacterium
	2	358	45.0	453	22	AAH66312	C glutamicum codin
c	3	358	45.0	349980	22	AAH68528	C glutamicum codin
	4	291	36.6	9407	23	AAS59606	Propionibacterium
c	5	266	33.4	4403765	22	AAI99683	Mycobacterium tube
c	6	266	33.4	4411529	22	AAI99682	Mycobacterium tube
c	7	209.5	26.3	651	24	ABK63022	Rat sequence diffe
c	8	201.5	25.3	349980	22	AAF86431	Pyrococcus abyssi
	9	196.5	24.7	849	22	AAH24909	Nucleotide sequenc
	10	196.5	24.7	873	22	AAK52120	Human polynucleoti
c	11	196.5	24.7	912	22	AAK53104	Human polynucleoti
	12	176.5	22.2	958	21	AAA02656	Human colon cancer
c	13	139.5	17.5	567	24	ABK54779	Human colon cancer
	14	102	12.8	21299	22	AAK89787	Human digestive sy
	15	96	12.1	6720	20	AAX13258	Enterococcus faeca
c	16	90.5	11.4	608	24	ABQ66323	Arabidopsis thalia
	17	90.5	11.4	648	21	AAC45058	Arabidopsis thalia
	18	90	11.3	1126	21	AAC36238	Arabidopsis thalia
	19	90	11.3	1186	21	AAC33853	Arabidopsis thalia
	20	90	11.3	1216	21	AAC33384	Arabidopsis thalia
	21	90	11.3	1217	21	AAC45391	Arabidopsis thalia
	22	89.5	11.2	651	21	AAC40420	Arabidopsis thalia
	23	89	11.2	1257	23	AAS54143	Pseudomonas aerugi
	24	88.5	11.1	482	20	AAX13281	Enterococcus faeca
	25	88.5	11.1	1766	19	AAV04490	Corn p-hydroxyphen
	26	88	11.1	1166	24	ABQ72545	Human MDDT encodin
	27	87.5	11.0	384	24	ABK73111	Bacillus lichenifo
	28	87.5	11.0	1555	23	ABL12133	Drosophila melanog
	29	86.5	10.9	291	24	ABK73137	Bacillus lichenifo
c	30	85	10.7	30159	23	AAS59564	Propionibacterium
	31	84.5	10.6	4770	23	ABL21665	Drosophila melanog
c	32	84.5	10.6	9718	23	ABL21664	Drosophila melanog
	33	84.5	10.6	1664976	19	AAV21209	Methanococcus jann

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2003, 12:39:53 ; Search time 139 Seconds
                                           (without alignments)
                                           1490.155 Million cell updates/sec

Title: US-09-942-407-2
Perfect score: 796
Sequence: 1 MSNEDLFICIDHVAYACPDA..........FMHPKSGKGVLIELTQYPKN 148

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US09942407/runat_04062003_144516_9495/app_query.fasta_1.32
7
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09942407_@CGN_1_1_57_@runat_04062003_144516_9495
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_NA:*
                 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                                    SUMMARIES
                           %
Result   Query
        No.   Score   Match Length DB   ID   Description
----
        1   796   100.0   447   10   US-09-942-407-1   Sequence 1, Appli
        2   358   45.0   453   9   US-09-738-626-1347   Sequence 1347, Ap
c   3   358   45.0 3309400   9   US-09-738-626-1   Sequence 1, Appli
c   4   209.5   26.3   651   10   US-09-917-800A-929   Sequence 929, App
        5   196.5   24.7   849   9   US-10-168-066-16   Sequence 16, Appl
        6   141.5   17.8   463   10   US-09-998-598-63   Sequence 63, Appl
c   7   139.5   17.5   567   10   US-09-919-580-249   Sequence 249, App
        8   137.5   17.3   1020   9   US-09-791-489-1   Sequence 1, Appli
        9   124   15.6   257   10   US-09-867-550-547   Sequence 547, App
        10   96   12.1   6720   10   US-09-070-927A-321   Sequence 321, App
        11   93   11.7   359   10   US-09-960-352-12234   Sequence 12234, A
        12   93   11.7   361   10   US-09-960-352-12770   Sequence 12770, A
c   13   90.5   11.4   608   10   US-09-770-149-900   Sequence 900, App
        14   89   11.2   1257   10   US-09-815-242-7780   Sequence 7780, Ap
        15   88.5   11.1   482   10   US-09-070-927A-344   Sequence 344, App
        16   87.5   11.0   384   10   US-09-974-300-402   Sequence 402, App
        17   86.5   10.9   291   10   US-09-974-300-428   Sequence 428, App
c   18   84   10.6   426   10   US-09-880-107-2065   Sequence 2065, Ap
        19   84   10.6   525   9   US-09-938-842A-1000   Sequence 1000, Ap
        20   84   10.6   797   10   US-09-770-445-828   Sequence 828, App
        21   82.5   10.4   885   9   US-09-938-842A-7   Sequence 7, Appli
        22   81.5   10.2   1854   9   US-09-738-626-475   Sequence 475, App
        23   81.5   10.2 3309400   9   US-09-738-626-1   Sequence 1, Appli
        24   80.5   10.1 1830121   9   US-10-329-960-1   Sequence 1, Appli
        25   79   9.9   49795   9   US-10-114-170-60   Sequence 60, Appl
        26   78   9.8   940   10   US-09-791-171-144   Sequence 144, App
        27   77.5   9.7   1338   9   US-09-938-842A-1440   Sequence 1440, Ap
        28   75.5   9.5   1488   10   US-09-815-242-4266   Sequence 4266, Ap
        29   75.5   9.5   1497   10   US-09-815-242-8237   Sequence 8237, Ap
        30   75.5   9.5   1536   10   US-09-815-242-6640   Sequence 6640, Ap
        31   75.5   9.5   5445   7   US-08-781-986A-73   Sequence 73, Appl
c   32   74.5   9.4   1867   9   US-09-888-320-1   Sequence 1, Appli
        33   73.5   9.2   627   10   US-09-974-300-6072   Sequence 6072, Ap
        34   73.5   9.2   2133   9   US-09-738-626-7   Sequence 7, Appli
c   35   72.5   9.1   1153   9   US-10-216-373-7   Sequence 7, Appli
        36   72.5   9.1   10322   7   US-08-781-986A-98   Sequence 98, Appl
c   37   72   9.0   2355   9   US-09-842-758-21   Sequence 21, Appl
c   38   71.5   9.0   10236   9   US-10-091-438-242   Sequence 242, App
c   39   71.5   9.0   10236   9   US-10-091-438-282   Sequence 282, App
        40   71.5   9.0   10236   10   US-09-764-853-878   Sequence 878, App
c   41   71   8.9   483   9   US-09-918-995-6609   Sequence 6609, Ap
        42   71   8.9   625   9   US-10-108-605-328   Sequence 328, App
        43   71   8.9   3060   9   US-10-210-965-3   Sequence 3, Appli

```
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OM protein - nucleic search, using frame_plus_p2n model

Run on:            June 10, 2003, 11:25:17 ; Search time 1235 Seconds
                                            (without alignments)
                                            1940.836 Million cell updates/sec

Title:             US-09-942-407-2
Perfect score:     796
Sequence:          1 MSNEDLFICIDHVAYACPDA..........FMHPKSGKGVLIELTQYPKN 148

Scoring table:     BLOSUM62
                   Xgapop 10.0 , Xgapext  0.5
                   Ygapop 10.0 , Ygapext  0.5
                   Fgapop  6.0 , Fgapext  7.0
                   Delop   6.0 , Delext   7.0

Searched:          16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters:       32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US09942407/runat_04062003_144515_9422/app_query.fasta_1.32
7
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09942407_@CGN_1_1_1906_@runat_04062003_144515_9422 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :         EST:*
                   1:  em_estba:*
                   2:  em_esthum:*
                   3:  em_estin:*
                   4:  em_estmu:*
                   5:  em_estov:*
                   6:  em_estpl:*
                   7:  em_estro:*
                   8:  em_htc:*
                   9:  gb_est1:*
                   10:  gb_est2:*
```

```
11:  gb_htc:*
12:  gb_est3:*
13:  gb_est4:*
14:  gb_est5:*
15:  em_estfun:*
16:  em_estom:*
17:  gb_gss:*
18:  em_gss_hum:*
19:  em_gss_inv:*
20:  em_gss_pln:*
21:  em_gss_vrt:*
22:  em_gss_fun:*
23:  em_gss_mam:*
24:  em_gss_mus:*
25:  em_gss_other:*
26:  em_gss_pro:*
27:  em_gss_rod:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	223.5	28.1	579	10	AW641355	AW641355 cm06e05.w
	2	223.5	28.1	679	10	AW635200	AW635200 bl30f06.w
	3	223.5	28.1	731	10	AW635277	AW635277 bl31f05.w
	4	210	26.4	587	13	BI594733	BI594733 As_tgz_43
c	5	209.5	26.3	570	9	AI411131	AI411131 EST239425
c	6	209.5	26.3	574	12	BF282550	BF282550 EST447141
c	7	209.5	26.3	651	9	AI172417	AI172417 EST218424
	8	209	26.3	582	13	BM356337	BM356337 kx63a05.y
	9	206	25.9	513	13	BM284249	BM284249 ki32a02.y
	10	206	25.9	541	13	BM284551	BM284551 ki60d01.y
	11	206	25.9	561	13	BM319066	BM319066 ki63h03.y
	12	206	25.9	563	13	BM281610	BM281610 ki18a01.y
	13	206	25.9	572	13	BM281475	BM281475 ki33f04.y
	14	206	25.9	576	13	BM281990	BM281990 ki24a01.y
	15	206	25.9	608	13	BM281639	BM281639 ki18c05.y
	16	206	25.9	610	13	BM284613	BM284613 kh97b03.y
	17	206	25.9	617	13	BM515300	BM515300 kj47c05.y
	18	206	25.9	625	13	BM283874	BM283874 ki28f05.y
	19	206	25.9	629	13	BM284117	BM284117 ki30b05.y
	20	206	25.9	631	13	BM566690	BM566690 kj04f11.y
	21	206	25.9	634	13	BM283587	BM283587 ki49d07.y
	22	206	25.9	652	13	BM569204	BM569204 kj45a11.y
	23	206	25.9	674	13	BM515150	BM515150 kj65a08.y
	24	204	25.6	599	13	BM514271	BM514271 kx98h01.y
	25	204	25.6	629	13	BM513752	BM513752 kx98h01.y
c	26	203.5	25.6	547	10	AW124555	AW124555 UI-M-BH2.
	27	203.5	25.6	570	9	AA220659	AA220659 my26e06.r
	28	203.5	25.6	688	11	AK003511	AK003511 Mus muscu
	29	203	25.5	577	13	BM283659	BM283659 ki50d12.y
c	30	202.5	25.4	535	10	AW987530	AW987530 uf25f04.x

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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 10, 2003, 11:55:02 ; Search time 46 Seconds
                                               (without alignments)
                                               986.699 Million cell updates/sec

Title: US-09-942-407-2
Perfect score: 796
Sequence: 1 MSNEDLFICIDHVAYACPDA..........FMHPKSGKGVLIELTQYPKN 148

Scoring table: BLOSUM62
                     Xgapop 10.0 , Xgapext 0.5
                     Ygapop 10.0 , Ygapext 0.5
                     Fgapop 6.0 , Fgapext 7.0
                     Delop   6.0 , Delext   7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US09942407/runat_04062003_144515_9466/app_query.fasta_1.32
7
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09942407_@CGN_1_1_40_@runat_04062003_144515_9466 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Issued_Patents_NA:*
                     1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                     2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                     3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                     4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                     5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                     6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	266	33.4	4403765	4	US-09-103-840A-2	Sequence 2, Appli
c	2	266	33.4	4411529	4	US-09-103-840A-1	Sequence 1, Appli
c	3	193	24.2	683	4	US-09-221-017B-170	Sequence 170, App
	4	83.5	10.5	33529	4	US-09-144-085-3	Sequence 3, Appli
	5	80.5	10.1	525	4	US-09-651-941-12	Sequence 12, Appl
	6	80.5	10.1	525	4	US-09-955-597-12	Sequence 12, Appl
	7	80.5	10.1	12508	4	US-09-655-270A-1	Sequence 1, Appli
	8	80.5	10.1	12523	4	US-09-651-941-1	Sequence 1, Appli
	9	80.5	10.1	12523	4	US-09-955-597-1	Sequence 1, Appli
	10	80	10.1	1206	4	US-09-153-599A-2	Sequence 2, Appli
	11	80	10.1	2299	4	US-09-153-599A-1	Sequence 1, Appli
	12	79	9.9	49795	4	US-09-453-702B-60	Sequence 60, Appl
	13	78	9.8	4403765	4	US-09-103-840A-2	Sequence 2, Appli
	14	78	9.8	4411529	4	US-09-103-840A-1	Sequence 1, Appli
	15	77.5	9.7	1338	4	US-08-945-515-2	Sequence 2, Appli
	16	77.5	9.7	1519	3	US-08-592-900-1	Sequence 1, Appli
	17	74.5	9.4	1287	4	US-09-134-001C-2042	Sequence 2042, Ap
	18	73.5	9.2	4163	4	US-09-004-838-70	Sequence 70, Appl
	19	73.5	9.2	4208	4	US-09-004-838-1	Sequence 1, Appli
c	20	73.5	9.2	4692	4	US-08-961-527-220	Sequence 220, App
c	21	72.5	9.1	1153	4	US-08-520-373D-7	Sequence 7, Appli
	22	72	9.0	1253	4	US-09-117-257-11	Sequence 11, Appl
	23	72	9.0	1253	4	US-08-945-476-11	Sequence 11, Appl
	24	72	9.0	1253	4	US-09-489-352-11	Sequence 11, Appl
	25	72	9.0	2653	2	US-08-589-711-1	Sequence 1, Appli
	26	72	9.0	2653	4	US-09-221-938-1	Sequence 1, Appli
	27	72	9.0	2653	4	US-08-945-476-7	Sequence 7, Appli
	28	72	9.0	2656	4	US-09-117-257-7	Sequence 7, Appli
	29	72	9.0	2656	4	US-09-489-352-7	Sequence 7, Appli
	30	71	8.9	1077	4	US-08-945-515-1	Sequence 1, Appli
	31	70	8.8	1723	4	US-09-199-637A-135	Sequence 135, App
	32	69.5	8.7	1329	4	US-08-945-515-3	Sequence 3, Appli
	33	69	8.7	1080	6	5474933-1	Patent No. 5474933
	34	69	8.7	45546	4	US-09-146-053-6	Sequence 6, Appli
	35	68.5	8.6	429	4	US-09-134-001C-636	Sequence 636, App
	36	68	8.5	1434	2	US-08-476-254-1	Sequence 1, Appli
	37	68	8.5	11444	2	US-08-222-617A-26	Sequence 26, Appl
	38	68	8.5	12364	2	US-08-222-617A-1	Sequence 1, Appli
c	39	67.5	8.5	525	4	US-08-858-207A-156	Sequence 156, App
c	40	67.5	8.5	1693	3	US-09-320-878-23	Sequence 23, Appl
c	41	67.5	8.5	1935	4	US-09-423-890-5	Sequence 5, Appli
c	42	67.5	8.5	5515	4	US-09-125-642C-8	Sequence 8, Appli
c	43	67.5	8.5	5519	4	US-09-125-642C-12	Sequence 12, Appl
	44	67.5	8.5	12047	2	US-09-022-461-1	Sequence 1, Appli
	45	67.5	8.5	12047	4	US-09-033-556-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-103-840A-2/c